

# SEQUENCE LISTING

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<110> Beamer, Lesa J.
      Eisenberg, David
      Carroll, Stephen F.

<120> BACTERICIDAL/PERMEABILITY-INCREASING PROTEIN:
      CRYSTALLIZATION, X-RAY DIFFRACTION, THREE-DIMENSIONAL
      STRUCTURE DETERMINATION, RATIONAL DRUG DESIGN AND
      MOLECULAR MODELING OF RELATED PROTEINS

<130> 11034US02

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<141> 2000-07-19

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Asp Asp Met Ile Pro Lys Glu Ser Lys Phe Arg Leu Thr Thr Lys Phe	
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Lys	Gly	Glu	Phe	Tyr	Ser	Glu	Asn	His	His	Asn	Pro	Pro	Pro	Phe	Ala	225	230	235	240
Pro	Pro	Val	Met	Glu	Phe	Pro	Ala	Ala	His	Asp	Arg	Met	Val	Tyr	Leu	245	250	255	
Gly	Leu	Ser	Asp	Tyr	Phe	Phe	Asn	Thr	Ala	Gly	Leu	Val	Tyr	Gln	Glu	260	265	270	
Ala	Gly	Val	Leu	Lys	Met	Thr	Leu	Arg	Asp	Asp	Met	Ile	Pro	Lys	Glu	275	280	285	
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Ser Thr Pro Pro His Leu Ser Val Gln Pro Thr Gly Leu Thr Phe Tyr  
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Pro Ala Val Asp Val Gln Ala Phe Ala Val Leu Pro Asn Ser Ser Leu  
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Ala Ser Leu Phe Leu Ile Gly Met His Thr Thr Gly Ser Met Glu Val  
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Ser Ala Glu Ser Asn Arg Leu Val Gly Glu Leu Lys Leu Asp Arg Leu  
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Leu Leu Glu Leu Lys His Ser Asn Ile Gly Pro Phe Pro Val Glu Leu  
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Leu Gln Asp Ile Met Asn Tyr Ile Val Pro Ile Leu Val Leu Pro Arg  
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Val Asn Glu Lys Leu Gln Lys Gly Phe Pro Leu Pro Thr Pro Ala Arg  
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Gly Arg Tyr Glu Phe His Ser Leu Asn Ile His Ser Cys Glu Leu Leu  
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His Ser Ala Leu Arg Pro Val Pro Gly Gln Gly Leu Ser Leu Ser Ile  
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Ser Asp Ser Ser Ile Arg Val Gln Gly Arg Trp Lys Val Arg Lys Ser  
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Phe	Phe	Lys	Leu	Gln	Gly	Ser	Phe	Asp	Val	Ser	Val	Lys	Gly	Ile	Ser		
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Ile	Ser	Val	Asn	Leu	Leu	Leu	Gly	Ser	Glu	Ser	Ser	Gly	Arg	Pro	Thr		
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Val	Thr	Ala	Ser	Ser	Cys	Ser	Ser	Asp	Ile	Ala	Asp	Val	Glu	Val	Asp		
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Tyr	Leu	Asn	Phe	Ser	Ile	Thr	Asp	Asp	Met	Ile	Pro	Pro	Asp	Ser	Asn		
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Arg	Leu	Tyr	Pro	Asn	Met	Asn	Leu	Glu	Leu	Gln	Gly	Ser	Val	Pro	Ser		
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Val	Phe	Arg	Leu	Ser	Val	Ala	Thr	Asn	Val	Ser	Ala	Thr	Leu	Thr	Phe		
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Asn	Thr	Ser	Lys	Ile	Thr	Gly	Phe	Leu	Lys	Pro	Gly	Lys	Val	Lys	Val		
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Ala Leu Leu Asn Tyr Tyr Ile Leu Asn Thr Phe Tyr Pro Lys Phe Asn  
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Asp Lys Leu Ala Glu Gly Phe Pro Leu Pro Leu Leu Lys Arg Val Gln  
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Ser Glu Val Lys Val Thr Glu Leu Gln Leu Thr Ser Ser Glu Leu Asp  
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Glu Leu Ser Arg Asp Pro Ala Gly Arg Met Lys Val Ser Asn Val Ser  
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Cys Gln Ala Ser Val Ser Arg Met His Ala Ala Phe Gly Gly Thr Phe  
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		275					280					285					
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Pro	Leu	Lys	Leu	Glu	Leu	Arg	Val	Leu	Ala	Pro	Pro	Arg	Cys	Thr	Ile		
305					310					315					320		
Lys	Pro	Ser	Gly	Thr	Thr	Ile	Ser	Val	Thr	Ala	Ser	Val	Thr	Ile	Ala		
				325					330					335			
Leu	Val	Pro	Pro	Asp	Gln	Pro	Glu	Val	Gln	Leu	Ser	Ser	Met	Thr	Met		
			340					345					350				
Asp	Ala	Arg	Leu	Ser	Ala	Lys	Met	Ala	Leu	Arg	Gly	Lys	Ala	Leu	Arg		
		355					360					365					
Thr	Gln	Leu	Asp	Leu	Arg	Arg	Phe	Arg	Ile	Tyr	Ser	Asn	His	Ser	Ala		
	370					375					380						
Leu	Glu	Ser	Leu	Ala	Leu	Ile	Pro	Leu	Gln	Ala	Pro	Leu	Lys	Thr	Met		
385					390					395					400		
Leu	Gln	Ile	Gly	Val	Met	Pro	Met	Leu	Asn	Glu	Arg	Thr	Trp	Arg	Gly		
				405					410					415			
Val	Gln	Ile	Pro	Leu	Pro	Glu	Gly	Ile	Asn	Phe	Val	His	Glu	Val	Val		
			420					425					430				
Thr	Asn	His	Ala	Gly	Phe	Leu	Thr	Ile	Gly	Ala	Asp	Leu	His	Phe	Ala		
	435						440					445					
Lys	Gly	Leu	Arg	Glu	Val	Ile	Glu	Lys	Asn	Arg	Pro	Ala	Asp	Val	Arg		
	450					455					460						
Ala	Ser	Thr	Ala	Pro	Thr	Pro	Ser	Thr	Ala	Ala	Val						
465					470					475							

<210> 6

<211> 470

<212> PRT

<213> Human

<220>

<223> cholesteryl ester transfer protein (CETP) (Figure 5)

<400> 6

His	Glu	Ala	Gly	Ile	Val	Cys	Arg	Ile	Thr	Lys	Pro	Ala	Leu	Leu	Val	1	5	10	15
Leu	Asn	His	Glu	Thr	Ala	Lys	Val	Ile	Gln	Thr	Ala	Phe	Gln	Arg	Ala	20	25	30	
Ser	Tyr	Pro	Asp	Ile	Thr	Gly	Glu	Lys	Ala	Met	Met	Leu	Leu	Gly	Gln	35	40	45	
Val	Lys	Tyr	Gly	Leu	His	Asn	Ile	Gln	Ile	Ser	His	Leu	Ser	Ile	Ala	50	55	60	
Ser	Ser	Gln	Val	Glu	Leu	Val	Glu	Ala	Lys	Ser	Ile	Asp	Val	Ser	Ile	65	70	75	80
Gln	Asn	Val	Ser	Val	Val	Phe	Lys	Gly	Thr	Leu	Lys	Tyr	Gly	Tyr	Thr	85	90	95	
Thr	Ala	Trp	Trp	Leu	Gly	Ile	Asp	Gln	Ser	Ile	Asp	Phe	Glu	Ile	Asp	100	105	110	
Ser	Ala	Ile	Asp	Leu	Gln	Ile	Asn	Thr	Gln	Leu	Thr	Cys	Asp	Ser	Gly	115	120	125	
Arg	Val	Arg	Thr	Asp	Ala	Pro	Asp	Cys	Tyr	Leu	Ser	Phe	His	Lys	Leu	130	135	140	
Leu	Leu	His	Leu	Gln	Gly	Glu	Arg	Glu	Pro	Gly	Trp	Ile	Lys	Gln	Leu	145	150	155	160
Phe	Thr	Asn	Phe	Ile	Ser	Phe	Thr	Leu	Lys	Leu	Val	Leu	Lys	Gly	Gln	165	170	175	
Ile	Cys	Lys	Glu	Ile	Asn	Val	Ile	Ser	Asn	Ile	Met	Ala	Asp	Phe	Val	180	185	190	
Gln	Thr	Arg	Ala	Ala	Ser	Ile	Leu	Ser	Asp	Gly	Asp	Ile	Gly	Val	Asp	195	200	205	
Ile	Ser	Leu	Thr	Gly	Asp	Pro	Val	Ile	Thr	Ala	Ser	Tyr	Leu	Glu	Ser	210	215	220	
His	His	Lys	Gly	His	Phe	Ile	Tyr	Lys	Asn	Val	Ser	Glu	Asp	Leu	Pro	225	230	235	240
Leu	Pro	Thr	Phe	Ser	Pro	Thr	Leu	Leu	Gly	Asp	Ser	Arg	Met	Leu	Tyr	245	250	255	
Phe	Trp	Phe	Ser	Glu	Arg	Val	Phe	His	Ser	Leu	Ala	Lys	Val	Ala	Phe	260	265	270	

Gln Asp Gly Arg Leu Met Leu Ser Leu Met Gly Asp Glu Phe Lys Ala  
 275 280 285

Val Leu Glu Thr Trp Gly Phe Asn Thr Asn Gln Glu Ile Phe Gln Glu  
 290 295 300

Val Val Gly Gly Phe Pro Ser Gln Ala Gln Val Thr Val His Cys Leu  
 305 310 315 320

Lys Met Pro Lys Ile Ser Cys Gln Asn Lys Gly Val Val Val Asn Ser  
 325 330 335

Ser Val Met Val Lys Phe Leu Phe Pro Arg Pro Asp Gln Gln His Ser  
 340 345 350

Val Ala Tyr Thr Phe Glu Glu Asp Ile Val Thr Thr Val Gln Ala Ser  
 355 360 365

Tyr Ser Lys Lys Lys Leu Phe Leu Ser Leu Leu Asp Phe Gln Ile Thr  
 370 375 380

Pro Lys Thr Val Ser Asn Leu Thr Glu Ser Ser Ser Glu Ser Ile Gln  
 385 390 395 400

Ser Phe Leu Gln Ser Met Ile Thr Ala Val Gly Ile Pro Glu Val Met  
 405 410 415

Ser Arg Leu Glu Val Val Phe Thr Ala Leu Met Asn Ser Lys Gly Val  
 420 425 430

Ser Leu Phe Asp Ile Ile Asn Pro Glu Ile Ile Thr Arg Asp Gly Phe  
 435 440 445

Leu Leu Leu Gln Met Asp Phe Gly Phe Pro Glu His Leu Leu Val Asp  
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Phe Leu Gln Ser Leu Ser  
 465 470

<210> 7  
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<220>  
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<210> 8  
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<220>

<223> BPI-54

<400> 8

gacagatctc tcgagtcatt tatagacaa

29

<210> 9

<211> 42

<212> DNA

<213> Human

<220>

<223> oligonucleotide from XcmI site to SphI site within  
BPI gene (encoding residues 348-361) containing  
the codon TCC for the serine at amino acid  
position 351

<400> 9

cccaactcct ccctggcttc cctcttcctg attggcatgc ac

42

<210> 10

<211> 42

<212> DNA

<213> Human

<220>

<223> Oligonucleotide complementary to SEQ ID NO:5

<400> 10

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42

<210> 11

<211> 14

<212> PRT

<213> Human

<220>

<223> "wild type" amino acid sequence of residues  
348-361 in BPI

<400> 11

Pro Asn Ser Ser Leu Ala Ser Leu Phe Leu Ile Gly Met His  
1 5 10

<210> 12

<211> 42

<212> DNA

<213> Human

<220>

<223> oligonucleotide from XcmI site to SphI site within  
the BPI gene (encoding residues 348-361)  
containing the codon GCC for alanine at amino acid  
position 351

<400> 12  
cccaactccg ccctggcttc cctcttcctg attggcatgc ac 42

<210> 13  
<211> 42  
<212> DNA  
<213> Human

<220>  
<223> Oligonucleotide complementary to SEQ ID NO:8

<400> 13  
gggttcaggc gggaccgaag ggagaaggac taaccgtacg tg 42

<210> 14  
<211> 14  
<212> PRT  
<213> Human

<220>  
<223> "nonglycosylated" amino acid sequence of residues  
348-361 in BPI

<400> 14  
Pro Asn Ser Ala Leu Ala Ser Leu Phe Leu Ile Gly Met His  
1 5 10